Available online at
www.agrospheresmagazine.com

ISSN: 2582 – 7022

Agrospheres:e-Newsletter, (2021) *2*(9), 42-45

Agrospheres™ e-Newsletter

Article ID: 292

Importance of Biotechnology in Sericulture Industry

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Article History
Received: 5. 09.2021
Revised: 16. 09.2021
Accepted: 24. 09.2021

INTRODUCTION

Sericulture is the science that deals with the production of qualitative and quantitative cocoons and silk by the rearing of silkworms. Silk is made up of fibroin and sericin protein of animal origin. It is also called the queen of textiles due to its softness, luster, elegance, tensile strength, and longer durability. The silkworm offers an excellent study material for breeding and genetic research by having innumerable visual and conspicuous characters, high fertility rate, and availability of several breeds in a year could be raised at will through the manipulation of environmental requirements, shorter life period, and capacity of males to mates several times. Biotechnology provides a great opportunity with better promise in sericulture. Taking awareness of the need to mix conventional breeding and modern biotechnological approaches to form sericulture economically viable the Central Silk Board (CSB), Ministry of Textiles (MOT), Govt. of India established Seri-Biotech Research Laboratory (SBRL) during 1993 in Bangalore. The main purpose of the application of biotechnology in the sericulture sector includes microinjection of DNA into eggs, cloning of silkworm hormones, transfer of genes conferring sturdiness, cloning of silk fibroin gene. Nowadays, recombinant DNA technology is a powerful application that can augment traditional strategies by improving the tool and cutting down time. Genetic engineering is another possible way that can be used for silkworm genetic improvement. Thus, concerted efforts are to be made to integrate conventional breeding with advanced technological development in silkworm for better sustainability and profitability of the silk industry in India.

Present status

In the recent past, the silkworm has become a model organism for understanding the biology of silkworms to manipulate and reconstruct the genes to produce high-quality silk. SBRL is a blend of conventional breeding and biotechnology tools. This institute has made significant contributions to the improvement of silk productivity through molecular breeding strategies both in silkworm and the host plant through various biotechnological approaches. Some of the significant findings include sex-linked markers, characterization of DNA markers, construction of early linkage maps, the establishment of stable germline transformation, production of pharmaceutically important proteins, immune response proteins, and annotation of thousands of expressed sequence tags (ESTs), construction of Bacterial Artificial Chromosome libraries (BACs), identification and characterization of Z chromosome linkage group, demonstration of lack of dosage compensation, the accomplishment of whole-genome sequencing, identification of W chromosome-specific BACs, Lepidoptera specific genes, horizontal gene transfer, and characterization of essential baculoviral genes. The development and improvement of the protocol of silkworm transgenesis have opened new areas of application. The nucleopolyhedrovirus is also being exploited as a vector for the introduction of foreign genes. Expression of marker proteins (luciferase and green fluorescent protein) has been successfully achieved in cell lines and larval caterpillars of silkworm (Bombyx mori) employing recombinant Bm NPV vector harboring reporter genes. Today, silkworm genetic manipulation is possible due to the availability of more than 400 visible mutations, 3000 diverse silkworm strains, high-density molecular linkage, and physical maps, the complete whole-genome sequence of 428 Mb, 16,000 expressed sequence tags (ESTs), and well-established transgenic system. Similarly, a PCR-based diagnostic technique has been developed for exclusive detection of transovarially and non-transovarially transmitted microsporidians that cause the deadly pebrine disease in silkworms.

Protein gene markers have been identified in mulberry silkworm (*Bombyx mori*) after uzi fly infection that can be utilized to screen *B.mori* germplasm for easy and accurate differentiation of immune-competent accessions within a short period. The induction of diapause in multivoltine *B.mori* eggs based on gene expression levels has been demonstrated leading to cost-effective conservation of multivoltine eggs up to six months without loss of quantitative characters. Molecular markers associated with the Muga line WWS1, SSR markers associated with the tasar silkworm ecotype Jatta, Daba that showed high divergence and genetic markers associated with altitude for the Lakhimpur eri silkworm population were identified which revealed the uniqueness of these lines proposing their conservation on priority as they are very useful for breed improvement. Nearly 28 SSR markers were developed for the characterization of diapausing and non-diapausing silkworms for higher and lower cocoon characters. ISSR markers identified that could outline fifteen eri silkworm populations with genetic homogeneity and less variability having a positive correlation of genetic distance with geographic distance and negative with an altitude between populations. The Indian isolate of Densovirus type 2 [DNV-2] was also identified which revealed high virulence and widespread occurrence under field conditions causing bacterial disease in *B. mori*. nsd-2 gene for resistance to DNV-2 was demonstrated to be useful in identifying DNV-2 resistant *B.mori* germplasm accessions for developing DNV-2 resistant breeds. Thirteen mulberry species were identified using Chloroplast DNA barcoding genes matK 390, matKMorus, trnL-F, and rbcL.

Prospects

Genomic maps constructed in standard silkworm strains using RFLPs, RAPD, ISSRs, STSs, and microsatellites have no doubt helped in stock identification, marker-assisted selection, identification of quantitative trait loci (QTL) characters. With the genomic interpretation of silkworms, even more laboratories around the world are going to be fascinated by its utilization. Further, efforts are intensified to spot traits for silk production more especially silk fibroin, sericin, disease resistance, etc. Possibilities of production of silkworm and their by-products and more especially their medical and biological usage through biotechnological methods should be explored. Characterization of useful traits of mulberry and non-mulberry silkworm through molecular tools are continuing with the available markers. Molecular markers can also be used to validate the parentage of individuals in a breeding population, for genetic 'finger-printing,' and protection of intellectual property rights. India is yet to reap the benefits of Seribiotechnology to bring out products in the form of technology as the same is still in the infant stage despite making sincere but compartmentalized attempts. The application of this technology has not only facilitated the functional analysis of silkworm genes, and enabled the sophisticated genetic modification of silkworms to improve their commercial characters, but also contributed to the development and use of similar technologies in non-model insects. Silk fiber used to produce fabrics and materials comes mainly from commercial silkworm species, and while conventional breeding practices have increased silk properties from individual silkworms, further increases using these methods have not been imminent. The modern genome modification and manipulation technologies hold great potential for creating novel commercial varieties by modifying endogenous genes or introducing exogenous genes. Genome modification technologies will allow the creation of novel silkworm species with increased yields and quality of silk, high resistance to virus, and other special properties. The silk gland is an ideal tissue for producing large quantities of valuable proteins and while several expression systems have been developed using the promoters of silk protein-encoding genes, improvements are required. First, silk protein production needs to be reduced or eliminated in strains of silkworms used for recombinant protein production. Silkworms are abundantly available in Asian countries and lots of laboratories have experienced rearing and maintaining larvae. Thus, the chance to utilize the long-forgotten resourceful silkworm for producing therapeutically important proteins, vaccines, and biomaterials is here. Understanding the hosts' protein mechanism will help in realizing more potential applications of this economic insect.

Recent progress within the field of sequencing and analysis has led to an incredible spike in data and therefore the development of knowledge science tools. One of the outcomes of this scientific progress is the development of various databases which are gaining popularity altogether in disciplines of biology including sericulture. As an economically important organism, silkworms are studied extensively for his or her numerous applications within the field of textiles, biomaterials, biomimetics, etc. Similarly, host plants, pests, pathogens, etc. are also being probed to understand the resources more efficiently. These studies have led to the generation of various seri-related databases which are extremely helpful for the scientific community.

The SilkDB, includes the genomic data, genome assembly, gene annotation, chromosomal mapping, orthologous relationship, and experiment data, like microarray expression data, Expressed Sequence Tags (ESTs), and corresponding references. Several new tools, including SilkMap, Silkworm Chromosome Browser (SCB), and BmArray, are developed to access silkworm genomic data conveniently. SilkDB is publicly available at the new URL of http://www.silkdb.org.

CONCLUSION

The status helps to integrate our focus on developing technologies targeted at the improvement of silkworm and host plants. Concerning the improvement of the silkworm, we need to emphasize the major diseases, their epidemiology for early detection of pathogens, pathogenicity, and pattern of host resistance as well as identification of markers for post cocoon traits such as denier, filament length, uniformity, tensile strength, etc. The improvement of silkworms should be based on shortlisting available silkworm germplasm races for various improved economic traits through the detection of respective DNA markers. Similarly, in the case of improvement of host plants, the focus should include tolerance to biotic and abiotic stresses as well as developing transgenic silkworms through the introgression of genes for stress tolerance and silkworm disease resistance. It is hoped that recent developments in silkworm genome research provide ample opportunities for silkworm geneticists and breeders to perform such an important task.

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